Gm50005.txt

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Payne, David
                 Lonsdale, John
                 Milner, Peter
                 Pearson, Stewart

(ii) TITLE OF INVENTION: FAB I

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:
   (A) ADDRESSEE: Dechert Price & Rhoads
   (B) STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
   (C) CITY: Philadelphia
   (D) STATE: PA
   (E) COUNTRY: US
   (F) ZIP: 19103

(v) COMPUTER READABLE FORM:
   (A) MEDIUM TYPE: Diskette
   (B) COMPUTER: IBM Compatible
   (C) OPERATING SYSTEM: Windows 95
   (D) SOFTWARE: FastSEQ for Windows Version 2.0b

(vi) CURRENT APPLICATION DATA:
   (A) APPLICATION NUMBER:
   (B) FILING DATE:
   (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
   (A) APPLICATION NUMBER: 60/024,845
   (B) FILING DATE: 28-AUG-1996

(viii) ATTORNEY/AGENT INFORMATION:
   (A) NAME: Falk, Stephen T
   (B) REGISTRATION NUMBER: 36,795
   (C) REFERENCE/DOCKET NUMBER: GM50005

(ix) TELECOMMUNICATION INFORMATION:
   (A) TELEPHONE: 215-994-2488
   (B) TELEFAX: 215-994-2222
   (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 771 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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ATGTTAAATC TTGAAAACAA AACATATGTC ATCATGGGAA TCGCTAATAA GCGTAGTATT
60
GCTTTTGGTG TCGCTAAAGT TTTAGATCAA TTAGGTGCTA AATTAGTATT TACTTACCGT    1
20
AAAGAACGTA GCCGTAAAGA GCTTGAAAAA TTATTAGAAC AATTAAATCA ACCAGAAGCG    1
80
CACTTATATC AAATTGATGT TCAAAGCGAT GAAGAGGTTA TTAATGGTTT TGAGCAAATT    2
40
GGTAAAGATG TTGGCAATAT TGATGGTGTA TATCATTCAA TCGCATTTGC TAATATGGAA    3
00
GACTTACGCG GACGCTTTTC TGAAACTTCA CGTGAAGGCT TCTTGTTAGC TCAAGACATT    3
60
AGTTCTTACT CATTAACAAT TGTGGCTCAT GAAGCTAAAA AATTAATGCC AGAAGGTGGT    4
20
AGCATTGTTG CAACAACATA TTTAGGTGGC GAATTCGCAG TTCAAAATTA TAATGTGATG    4
80
GGTGTTGCTA AAGCGAGCTT AGAAGCAAAT GTTAAATATT TAGCATTAGA CTTAGGTCCT    5
40
GATAATATTC GCGTTAATGC AATTTCAGCT GGTCCAATCC GTACATTAAG TGCAAAAGGT    6
00
GTGGGTGGTT TCAATACAAT TCTTAAAGAA ATCGAAGAGC GTGCACCTTT AAAACGTAAC    6
60
GTTGATCAAG TAGAAGTAGG TAAAACAGCG GCTTACTTRT TAAGTGACTT ATCAAGTGGC    7
20
GTTACAGGTG AAAATATTCA TGTAGATAGC GGATTCCACG CAATTAAATA A              7
71
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(2) INFORMATION FOR SEQ ID NO:2:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 256 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Leu Asn Leu Glu Asn Lys Thr Tyr Val Ile Met Gly Ile Ala Asn

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1               5                   10                  15
Lys Arg Ser Ile Ala Phe Gly Val Ala Lys Val Leu Asp Gln Leu Gly
                            20              25              30
Ala Lys Leu Val Phe Thr Tyr Arg Lys Glu Arg Ser Arg Lys Glu Leu
            35              40              45
Glu Lys Leu Leu Glu Gln Leu Asn Gln Pro Glu Ala His Leu Tyr Gln
            50              55              60
Ile Asp Val Gln Ser Asp Glu Glu Val Ile Asn Gly Phe Glu Gln Ile
65              70              75              80
Gly Lys Asp Val Gly Asn Ile Asp Gly Val Tyr His Ser Ile Ala Phe
                85              90              95
Ala Asn Met Glu Asp Leu Arg Gly Arg Phe Ser Glu Thr Ser Arg Glu
            100             105             110
Gly Phe Leu Leu Ala Gln Asp Ile Ser Ser Tyr Ser Leu Thr Ile Val
            115             120             125
Ala His Glu Ala Lys Lys Leu Met Pro Glu Gly Gly Ser Ile Val Ala
            130             135             140
Thr Thr Tyr Leu Gly Gly Glu Phe Ala Val Gln Asn Tyr Asn Val Met
145             150             155             160
Gly Val Ala Lys Ala Ser Leu Glu Ala Asn Val Lys Tyr Leu Ala Leu
                165             170             175
Asp Leu Gly Pro Asp Asn Ile Arg Val Asn Ala Ile Ser Ala Gly Pro
            180             185             190
Ile Arg Thr Leu Ser Ala Lys Gly Val Gly Gly Phe Asn Thr Ile Leu
            195             200             205
Lys Glu Ile Glu Glu Arg Ala Pro Leu Lys Arg Asn Val Asp Gln Val
            210             215             220
Glu Val Gly Lys Thr Ala Ala Tyr Leu Leu Ser Asp Leu Ser Ser Gly
225             230             235             240
Val Thr Gly Glu Asn Ile His Val Asp Ser Gly Phe His Ala Ile Lys
            245             250             255
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